

**BEST AVAILABLE COPY**

25	891.8	60.3	1517	3	US-09-554-106-2	Sequence 2, Appl1
26	891.8	60.3	1517	3	US-09-554-106-2	Sequence 2, Appl1
27	889.2	60.1	1516	3	US-09-248-528-3	Sequence 3, Appl1
28	889.2	60.1	1516	3	US-09-549-108-3	Sequence 3, Appl1
29	889.2	60.1	1516	3	US-09-549-111-3	Sequence 3, Appl1
30	889.2	60.1	1516	3	US-09-549-106-3	Sequence 3, Appl1
31	889.2	60.1	1516	3	US-09-550-394-3	Sequence 3, Appl1
32	889.2	60.1	1516	3	US-09-426-868-1	Sequence 1, Appl1
33	885.2	59.9	1539	3	US-09-938-035B-1	Sequence 1, Appl1
34	883.4	59.7	1539	3	US-09-938-035B-2	Sequence 2, Appl1
35	882.8	59.7	1547	3	US-10-296-1319-1	Sequence 1, Appl1
36	877.4	59.3	1542	3	US-08-956-960-2	Sequence 2, Appl1
37	876.4	59.3	1567	3	US-09-375-922A-4	Sequence 4, Appl1
38	876.4	59.3	1567	3	US-10-155-562A-4	Sequence 4, Appl1
39	871.6	58.9	1540	3	US-09-228-184-1	Sequence 1, Appl1
40	871.6	58.9	1540	3	US-09-967-376-1	Sequence 1, Appl1
41	869	58.8	3169	3	US-09-710-279-3356	Sequence 3356, Appl1
42	869	58.8	3308	3	US-09-710-279-3905	Sequence 3905, Appl1
43	868.2	58.7	1555	2	US-08-757-653-160	Sequence 160, Appl1
44	868.2	58.7	1555	2	US-08-522-946-160	Sequence 160, Appl1
45	868.2	58.7	1555	3	US-09-653-378A-160	Sequence 160, Appl1

## ALIGNMENTS

```

RESULT 1
US-10-085-871C-2
; Sequence 2, Application US/10085871C
; Patent No. 6716615
; GENERAL INFORMATION:
; APPLICANT: Lee, Pang-yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Shung-ching
; TITLE OF INVENTION: New Strains of Saccharothrix, Process for Producing Pravaastatin
; TITLE OF INVENTION: Strains and Isolation Process of (HMG)-COA Reductase
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/085,871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Saccharothrix 45494
US-10-085-871C-2

```

Query match	84.5%;	Score 1250.4;	DB 3;	Length 1471.
-------------	--------	---------------	-------	--------------

Matches 1342; Conservative 0; Mismatches 116; Indels 2; Gaps 2;

Qy	21	GAGGAACGGCTGGCCGGCGTGTCTTAACACATGCAAGTCGAGCGGAAAGGCCCTTTCGGGGTAC	80
Db	1	GAGGAACGGCTGGCCGGCGTGTCTTAACACATGCAAGTCGAGCGGTAAAGGCCCTTTCGGGGTAC	60
Qy	81	TCGAGGGGGGAAACGGGTGAGTAAACAAGAGTAACCTGGCCAGGCTTGGGATTAACCCC	140
Db	61	ACGAGCGGGGAAACGGGTGAGTAAACAAGAGTAACCTGGCTGTAACTCCGGGATTAACCTT	120
Qy	141	GGGAACCGGGGCTAATACCGGATATGACCATCTGTGCGATGTGGGTGTGGAAAGATT	200
Db	121	GGGAACCTGAGGCTTAATACCGGATATGACCCCAATAGGCACTTGTGGGTGTGGAAAGTTTC	180
Qy	201	TTTGTGCTTGGGATGGGCTCGCGGCTTAATCACTGTGTGGGTGATGGCTTAACCAAG	260
Db	181	CGCGGGTATGGGATGGGACCCCGGCGCTTAATCACTTGTGTGGGTGATGGCTTAACCAAG	240
Qy	261	GGCGGCAACGGGTATAGCCGCTGAGAGGGCGAACCGGCAACTGGGAATGAGAACAGCGCCC	320
Db	241	GGCAACCAACGGGTATAGCCGCTGAGAGGGGTAGACCGGCAACTGGGAATCTAGAACACCGCCC	300
Qy	321	AGACTCTTAACGGAGAGCGACAGTGGGGAAATCTTGCAACAATGGGCGAAGCCTTAGTCAGC	380

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# OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:15:50 ; Search time 6468 seconds  
(without alignments)  
10698.530 Million cell updates/sec

Title: US-09-991-518C-4  
Perfect score: 1479  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 2339354128 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:

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4: gb\_hcc:\*  
5: gb\_esc4:\*  
6: gb\_esc5:\*  
7: gb\_esc6:\*  
8: gb\_esc7:\*  
9: gb\_gsa1:\*  
10: gb\_gsa2:\*  
11: gb\_gsa3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	817	55.2	6499	9	BH771024 LLMGtag74
2	753.6	51.0	1954	7	CX109203 RECM0593
3	752.2	50.9	874	7	CO365133 RTK1.23.G
4	705.2	47.7	887	10	CL693661 PRI0167a
5	607.6	41.1	1053	9	BZ447500 BONK40TR
6	606.8	41.0	1084	9	BZ439740 BONND54TR
7	594.8	40.2	1077	9	BZ450751 BONB063TR
8	594.6	40.2	744	9	BZ781734 I131B08.G
9	593	40.1	1079	9	BH705272 BOMK286TR
10	592.6	40.1	1031	9	BH656222 BOMK477TR
11	587.6	39.7	1010	9	BZ431523 BONHD88TR
12	583.4	39.4	1016	9	BZ426201 BONND28TR
13	577.2	39.0	1044	9	BZ463550 BONKCR6TR
14	573.4	38.8	1051	9	BZ494182 BONKRS4TR
15	571.6	38.6	1054	9	BH647750 BONMD31TR
16	557.4	37.7	663	6	CD096847 ME1-0010T
17	552.4	37.3	974	9	BZ440868 BONKTS1TR
18	552.2	37.3	1106	9	BZ469058 BONHBS4TR
19	551.6	37.3	1069	9	BZ474941 BONKRS9TR
20	543.8	36.8	725	7	CN204148 TOR4539.G
21	543	36.7	899	9	BZ685785 PUBDR54TR
22	542.4	36.7	977	9	BZ459232 BONKQ28TR

23	542.2	36.7	762	8	DR385950 RTKG1.11
24	536.8	36.3	951	9	BH651765 BOMPE30TR
25	527.4	35.7	1050	10	CM001852 ZMMBHG000
26	526.8	35.6	885	7	CN201712 TOR1780.G
27	523.8	35.4	947	9	BZ464837 BONKPT6TR
28	522	35.3	1096	9	BZ502068 BONI125TR
29	520.6	35.2	918	9	BZ437960 BONNV72TR
30	518.6	35.1	901	9	BZ461852 BONKO15TR
31	517.8	35.0	617	6	CD096968 ME1-0011T
32	516.4	34.9	915	7	CV287759 aof01-13m
33	515.6	34.9	875	7	CV292617 aof01-2ms
34	511.6	34.6	1082	9	BZ459110 BONBR59TR
35	505.4	34.2	862	9	BH527452 BOGVP36TR
36	505	34.1	1030	9	BZ463792 BONKY05TR
37	504.6	34.1	895	8	DR027023 Osmo01058
38	504	34.1	889	9	BZ426275 BOOAB81TR
39	502.8	34.0	1020	9	BH685417 BOMG90TR
40	501.2	33.9	940	11	CT016030 KBPH125K2
41	501.2	33.9	955	11	CT013781 KBPH122A0
42	500.8	33.9	935	9	BZ468986 BONND78TR
43	500.8	33.9	950	7	CK285891 EST748613
44	499.8	33.8	995	9	BH700021 BONMD50TR
45	498.4	33.7	837	7	CV291378 aof01-1ms

## ALIGNMENTS

RESULT 1  
LOCUS BH771024 6499 bp DNA linear GSS 01-MAY-2002  
DEFINITION LLMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, genomic survey sequence.

ACCESSION BH771024  
VERSION BH771024.1 GI:20373981  
KEYWORDS GSS.  
SOURCE Lactococcus lactis subsp. cremoris  
ORGANISM Lactococcus lactis subsp. cremoris  
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
Lactococcus.

REFERENCE 1 (bases 1 to 6499)  
AUTHORS Boletín, A., Ehrlich, S. D. and Sorokin, A.  
JOURNAL Studies of genomes of dairy bacteria Lactococcus lactis Sci. Alimentis (2002) In press  
COMMENT Contact: Sorokin, A  
Genetique Microbiome

## INRA

CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France  
Tel: 33 1 34 65 25 16  
Fax: 33 1 34 65 25 21

Email: sorokin@jouy.inra.fr  
best homologue in strain I11403 is ywga (78%)

Class: shotgun

High quality sequence start: 30  
High quality sequence stop: 6471.

## FEATURES

location/Qualifiers

1..6499  
/organism="Lactococcus lactis subsp. cremoris"  
/mol\_type="genomic DNA"  
/strain="MG1363"  
/sub\_species="cremoris"  
/db\_xref="taxon:1359"  
/clone\_lib="MG1363 Random Sequence Tag Library"  
/note="Vector: pSGM2; Site 1: Small; Library of chromosomal fragments of L. lactis strain MG1363 was prepared by partial AluI digestion or by sonication."

## ORIGIN

Query Match 55.2%; Score 817, DB 9; Length 6499;  
Best Local Similarity 75.6%; Pred. No. 3.6e-215; Indels 45; Gaps 9;  
Matches 1147; Conservative 0; Mismatches 325;

1 AGAGTTTATCTGCTCAGGACGAAACGCTGCGCGCTGCTTAACACATGCAAGTCGAGC 60

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:12:04 ; Search time 1667 Seconds  
(without alignments)  
5913.066 Million cell updates/sec

Title: US-09-991-518C-4

Sequence: 1 agagcttgatcctgcgtcag.....agctgaacaagtgacgcgt 1479

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: geneeqn1990s:\*
- 3: geneeqn2000s:\*
- 4: geneeqn2001as:\*
- 5: geneeqn2001bs:\*
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- 7: geneeqn2002bs:\*
- 8: geneeqn2003as:\*
- 9: geneeqn2003bs:\*
- 10: geneeqn2003cs:\*
- 11: geneeqn2003ds:\*
- 12: geneeqn2004as:\*
- 13: geneeqn2004bs:\*
- 14: geneeqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1330.6	90.0	1440	14	ADZ35975 Verrucos1
2	1283.6	86.8	1403	12	ADJ38609 Micromono
3	1261.6	85.3	1514	14	ADW12667 Rhodococc
4	1255.2	84.9	1511	13	ADR90325 Rhodococc
5	1251.4	84.6	1488	13	ADG17269 Lechevrai1
6	1250.4	84.5	1471	12	ADP56671 YS-45494
7	1250.4	84.5	1471	12	ADG64520 Saccharot
8	1250.4	84.5	1471	14	ADY86148 Saccharot
9	1235.2	83.5	1480	3	AAA40374 Rhodococc
10	1235.2	83.5	1480	3	AAA40373 Rhodococc
11	1235	83.5	1517	12	ADM92517 Gordonia
12	1235	83.5	1517	12	ADQ1823 DNA of RN
13	1229.6	83.1	1511	13	ADR90327 Rhodococc
14	1228.4	83.1	1437	12	ADP56670 YS-44442
15	1228.4	83.1	1437	12	ADG64519 Saccharot
16	1228.4	83.1	1437	14	ADY86147 Saccharot
17	1223.8	82.7	1482	14	AEA22404 Mycobacte
18	1220	82.5	1455	14	AEA22412 Mycobacte
19	1219	82.4	1492	14	ADZ69170 Marine ac

20	1217.4	82.3	1492	14	ADZ69171 Marine ac
21	1213.6	82.1	1514	13	ADR90326 Rhodococc
22	1211	81.9	1492	14	ADZ69172 Marine ac
23	1208.2	81.7	1457	6	ABN86275
24	1206.2	81.6	1457	6	ABN86276
25	1194.8	80.8	1449	14	AEA22405 Mycobacte
26	1192	80.6	1474	14	ADZ69169 Marine ac
27	1188.8	80.4	1524	11	ABR80307 Organic w
28	1185	80.1	1525	11	ABR80304 Organic w
29	1183.8	80.0	1464	14	AEA22414 Mycobacte
30	1180	79.8	1452	2	AAK82004
31	1177.2	79.6	1443	14	ADX38843 Microbiop
32	1175.6	79.5	1517	11	ABR80305 Organic w
33	1172	79.2	2743	2	AAO37639 Mycobacte
34	1168.2	79.0	2743	4	AAK59540 Propionib
35	1168.2	79.0	2743	8	ACF64469 Propionib
36	1166.8	78.9	1439	14	AEA22403 Mycobacte
37	1166.8	78.9	1524	4	AAK30719 Mycobacte
38	1166.8	78.9	1536	10	ADB61681 16S rRNA
39	1166.8	78.9	1537	10	ADP41649 Mycobacte
40	1166.8	78.9	1537	10	ADP41649 Mycobacte
41	1166.8	78.9	110000	4	AAI99682_14 Continuation (15 o
42	1166.8	78.9	110000	4	AAI99682_14 Continuation (15 o
43	1161.6	78.5	1508	14	ADZ69174 Marine ac
44	1161.4	78.5	1503	14	ADZ69173 Marine ac
45	1153.6	78.0	1461	14	AEA22406 Mycobacte

#### ALIGNMENTS

RESULT 1	ADZ35975	standard; DNA; 1440 BP.
ID	ADZ35975	standard; DNA; 1440 BP.
AC	ADZ35975;	
DT	30-JUN-2005	(first entry)
XX	Verrucos1spora sp. AB-18-032 16S rRNA gene.	
XX	ds; antibiotic; antimetabolic; protozoacide; 16S rRNA;	
XX	polycyclic macrolactone; abysomycin; p-Aminobenzoic acid; folic acid;	
XX	vitamin; abysomycin B; abysomycin C; abysomycin D;	
XX	Staphylococcus aureus infection; protozoal infection;	
XX	plasmidial infection; Leishmania infection; Chagas disease;	
XX	Gram positive bacteria infection; mrsa infection .	
OS	Verrucos1spora sp. AB-18-032.	
PN	MO200503114-A1.	
PN	14-APR-2005.	
PP	23-SEP-2004; 2004KO-EP010661.	
PR	01-OCT-2003; 2003DR-01047472.	
PR	11-NOV-2003; 2003DR-01053300.	
PA	(UVTU-) UNIV TUEBINGEN.	
XX	Fiedler H, Suesmuth R, Zaehner H, Bull A;	
XX	WPI; 2005-296122/30.	
XX	New abysomycin polycyclic macrolactone compounds, useful as antibiotics	
XX	and antiprotzoal agents effective against multiresistant strains,	
XX	prepared using bacteria of genus Verrucos1spora.	
XX	Disclosure; SEQ ID NO 1; 47pp; German.	
CC	This invention describes novel polycyclic macrolactones and their	
CC	derivatives , prepared using bacteria of genus Verrucos1spora and	

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OM nucleic - nucleic search, using SW model

Run on: April 15, 2006, 22:09:44 ; Search time 7424 Seconds

(without alignments)  
11324.281 Million cell updates/sec

Title: US-09-991-518c-4

Perfect score: 1479

Sequence: 1 agagcttgatccctggctcag.....agtcgtaacagtagccgc 1479

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pi:\*

9: gb\_ro:\*

10: gb\_scs:\*

11: gb\_sy:\*

12: gb\_un:\*

13: gb\_vl:\*

14: gb\_hcg:\*

15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1479	100.0	1479	1	AY040619 Salinospo
2	1479	100.0	1479	1	AY040620 Salinospo
3	1479	100.0	1479	1	AY040621 Salinospo
4	1479	100.0	1479	1	AY040622 Salinospo
5	1479	99.9	1479	1	AY040623 Salinospo
6	1479	99.9	1479	1	AY040624 Salinospo
7	1479	99.9	1479	1	AY040625 Salinospo
8	1479	99.9	1479	1	AY040626 Salinospo
9	1479	99.9	1479	1	AY040627 Salinospo
10	1479	99.9	1479	1	AY040628 Salinospo
11	1479	99.9	1479	1	AY040629 Salinospo
12	1479	99.9	1479	1	AY040630 Salinospo
13	1479	99.9	1479	1	AY040631 Salinospo
14	1479	99.9	1479	1	AY040632 Salinospo
15	1479	99.9	1479	1	AY040633 Salinospo
16	1479	99.9	1479	1	AY040634 Salinospo
17	1479	99.9	1479	1	AY040635 Salinospo
18	1479	99.9	1479	1	AY040636 Salinospo

19	1459	98.6	1480	1	AY562200 Salinospo
20	1454	98.3	1479	1	AY562203 Salinospo
21	1429	96.6	1429	1	AY878316 Salinospo
22	1414.2	95.6	38146	1	AY524043 Micromono
23	1409.4	95.3	1479	1	AY040625 Micromono
24	1405.8	95.1	1507	1	AB193564 Micromono
25	1405.8	95.1	1508	1	AB193563 Micromono
26	1404.6	95.0	1508	1	AB193562 Micromono
27	1403.6	94.9	1482	1	AB159779 Micromono
28	1403	94.9	1470	1	MMRN165 Micromono
29	1402.4	94.8	1476	1	MC116SRN Micromono
30	1401.8	94.8	1476	1	MC116SRN Micromono
31	1401.4	94.8	1479	1	AY040624 Micromono
32	1400.8	94.7	1471	1	MEP16SRN Micromono
33	1400.2	94.7	1474	1	MEP16SRN Micromono
34	1400.2	94.7	1476	1	MEP16SRN Micromono
35	1399.8	94.6	1480	1	AY534920 Micromono
36	1399.4	94.6	1477	1	MEN560635 Micromono
37	1399	94.6	1466	1	MERN165 Micromono
38	1399	94.6	1466	1	MERN165 Micromono
39	1398.6	94.6	1477	1	MAU245712 Micromono
40	1398.6	94.6	1477	1	MRO16SRN Micromono
41	1396.6	94.4	1509	1	AJ783989 Micromono
42	1396.6	94.4	1509	1	AJ783992 Micromono
43	1396.6	94.4	1510	1	AJ783994 Micromono
44	1396	94.4	1472	1	MEB16SRN Micromono
45	1395.4	94.3	1476	1	NML6RRA Micromono

## ALIGNMENTS

RESULT 1	AY040619	AY040619	1479 bp	DNA	linear	BCT 08-JUN-2005
LOCUS	AY040619	AY040619	1479 bp	DNA	linear	BCT 08-JUN-2005
DEFINITION	Salinospora sp. CNH643 16S ribosomal RNA gene, partial sequence.	AY040619				
ACCESSION	AY040619					
VERSION	AY040619.2	GI:67043491				
KEYWORDS						
SOURCE						
ORGANISM	Salinospora arenicola					
REFERENCE	1 (bases 1 to 1479)					
AUTHORS	Mincer, T.J., Jensen, P.R., Kaufman, C.A. and Fenical, W.					
TITLE	Widespread and persistent populations of a major new marine actinomycete taxon in ocean sediments					
JOURNAL	Appl. Environ. Microbiol. 68 (10), 5005-5011 (2002)					
PUBMED	12324350					
REFERENCE	2 (bases 1 to 1479)					
AUTHORS	Mincer, T.J., Jensen, P.R., Kaufman, C.A. and Fenical, W.					
TITLE	Direct Submission					
JOURNAL	Submitted (15-JUN-2001) Marine Chemistry, Scripps Institution of Oceanography, UCSD, 8602 La Jolla Shores Dr., La Jolla, CA 92093-0204, USA					
REFERENCE	3 (bases 1 to 1479)					
AUTHORS	Jensen, P.R., Mincer, T.J. and Fenical, W.					
TITLE	Direct Submission					
JOURNAL	Submitted (08-JUN-2005) CNMB, Scripps Institution of Oceanography, Mail Code 0204, La Jolla, CA 92093, USA					
REMARK	Sequence update by submitter					
COMMENT	On Jun 8, 2005 this sequence version replaced gi:22474336.					
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ORIGIN	/strain="CNH643"					
ORIGIN	/db_xref="taxon:168697"					
ORIGIN	<1..51479					
ORIGIN	/product="16S ribosomal RNA"					
ORIGIN	Query Match					
ORIGIN	100.0%; Score 1479; DB 1; Length 1479;					

Sun Apr 16 12:42:18 2006

us-09-991-5

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OM nucleic - nucleic search, using sw model

Run on: April 16, 2006, 00:04:50 ; Search time 788 Seconds  
(without alignments)  
7559.850 Million cell updates/sec

Title: US-09-991-518C-4  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:\*  
1: /SIDSS/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
2: /SIDSS/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /SIDSS/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /SIDSS/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
5: /SIDSS/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
6: /SIDSS/ptodata/2/pubpna/US09\_NEW\_PUB.seq1:\*  
7: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
8: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq1:\*  
9: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq2:\*  
10: /SIDSS/ptodata/2/pubpna/US10\_NEW\_PUB.seq3:\*  
11: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
12: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*  
13: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq3:\*  
14: /SIDSS/ptodata/2/pubpna/US11\_NEW\_PUB.seq4:\*  
15: /SIDSS/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:35:29 ; Search time 524 Seconds  
(without alignments)  
8702.075 Million cell updates/sec

Title: US-09-991-518C-4  
Perfect score: 1479  
Sequence: 1 agagtttgatcctggctcag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6753657 seqs, 1541544009 residues

Total number of hits satisfying chosen parameters: 13507314

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_NA New:\*

- 1: /SIDS5/ptodata/2/pna/PCT\_NEW\_COMB.seq:\*
- 2: /SIDS5/ptodata/2/pna/US06\_NEW\_COMB.seq:\*
- 3: /SIDS5/ptodata/2/pna/US07\_NEW\_COMB.seq:\*
- 4: /SIDS5/ptodata/2/pna/US08\_NEW\_COMB.seq:\*
- 5: /SIDS5/ptodata/2/pna/US09\_NEW\_COMB.seq:\*
- 6: /SIDS5/ptodata/2/pna/US10\_NEW\_COMB.seq:\*
- 7: /SIDS5/ptodata/2/pna/US10\_NEW\_COMB.seq1:\*
- 8: /SIDS5/ptodata/2/pna/US11\_NEW\_COMB.seq:\*
- 9: /SIDS5/ptodata/2/pna/US11\_NEW\_COMB.seq1:\*
- 10: /SIDS5/ptodata/2/pna/US11\_NEW\_COMB.seq2:\*
- 11: /SIDS5/ptodata/2/pna/US11\_NEW\_COMB.seq3:\*
- 12: /SIDS5/ptodata/2/pna/US60\_NEW\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1183.6	80.0	1487	8	US-11-335-686-1	Sequence 1, Appli
2	1177.2	79.6	1443	7	US-10-521-336-1	Sequence 1, Appli
3	869.6	58.8	2944528	10	US-11-045-004-1	Sequence 1, Appli
c 4	869.6	58.8	2944528	10	US-11-045-004-1	Sequence 1, Appli
5	868.2	58.7	1555	5	US-09-941-095-160	Sequence 160, App
6	865.4	58.5	1554	11	US-11-348-413-10825	Sequence 10825, A
7	863.6	58.4	1504	10	US-11-273-617-10	Sequence 10, Appl
8	858	58.0	1587	10	US-11-273-617-8	Sequence 8, Appli
9	851.8	57.6	1538	11	US-11-348-413-12	Sequence 12, Appl
10	851.8	57.6	1541	8	US-11-370-472-18	Sequence 18, Appl
11	850.2	57.5	1513	8	US-11-370-472-10	Sequence 10, Appl
12	845.8	57.2	1540	8	US-11-370-472-30	Sequence 30, Appl
13	845.4	57.2	1541	8	US-11-370-472-19	Sequence 19, Appl
14	843.8	57.1	1550	8	US-11-370-472-64	Sequence 64, Appl
15	843.8	57.1	1550	8	US-11-370-472-65	Sequence 65, Appl
16	843.8	57.1	1550	8	US-11-370-472-66	Sequence 66, Appl
17	843.8	57.1	1550	8	US-11-370-472-67	Sequence 67, Appl
18	843.8	57.1	1550	8	US-11-370-472-68	Sequence 68, Appl
19	843.8	57.1	1550	8	US-11-370-472-69	Sequence 69, Appl
20	843.8	57.1	2160266	7	US-10-513-024-1373	Sequence 1373, Ap
21	843.2	57.0	1568	10	US-11-273-617-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:19:09 / Search time 8961 Seconds  
(without alignments)  
9125.795 Million cell updates/sec

Title: US-09-991-518c-4  
Perfect score: 1479  
Sequence: 1 agatgttgatccctgctcag.....agtcgtacaaaggtacgct 1479

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues  
Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Pending Patents NA Main:\*

- 1: /cgn2\_6/ptodata/1/pna/US081\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pna/US082\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pna/US083\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pna/US084\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pna/US085\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pna/US086\_COMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pna/US087\_COMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pna/US088\_COMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pna/US089\_COMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pna/US090\_COMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pna/US091\_COMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pna/US092\_COMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pna/US093\_COMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pna/US094\_COMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pna/US095\_COMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pna/US096\_COMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pna/US097\_COMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pna/US098\_COMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pna/US099\_COMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pna/US100\_COMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pna/US101\_COMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pna/US102\_COMB.seq:\*
- 23: /cgn2\_6/ptodata/1/pna/US103\_COMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pna/US104\_COMB.seq:\*
- 25: /cgn2\_6/ptodata/1/pna/US105\_COMB.seq:\*
- 26: /cgn2\_6/ptodata/1/pna/US106\_COMB.seq:\*
- 27: /cgn2\_6/ptodata/1/pna/US107\_COMB.seq:\*
- 28: /cgn2\_6/ptodata/1/pna/US108\_COMB.seq:\*
- 29: /cgn2\_6/ptodata/1/pna/US109\_COMB.seq:\*
- 30: /cgn2\_6/ptodata/1/pna/US110\_COMB.seq:\*
- 31: /cgn2\_6/ptodata/1/pna/US111\_COMB.seq:\*
- 32: /cgn2\_6/ptodata/1/pna/US112\_COMB.seq:\*
- 33: /cgn2\_6/ptodata/1/pna/US113\_COMB.seq:\*
- 34: /cgn2\_6/ptodata/1/pna/US114\_COMB.seq:\*
- 35: /cgn2\_6/ptodata/1/pna/US115\_COMB.seq:\*
- 36: /cgn2\_6/ptodata/1/pna/US116\_COMB.seq:\*
- 37: /cgn2\_6/ptodata/1/pna/US117\_COMB.seq:\*
- 38: /cgn2\_6/ptodata/1/pna/US118\_COMB.seq:\*
- 39: /cgn2\_6/ptodata/1/pna/US119\_COMB.seq:\*
- 40: /cgn2\_6/ptodata/1/pna/US120\_COMB.seq:\*
- 41: /cgn2\_6/ptodata/1/pna/US121\_COMB.seq:\*
- 42: /cgn2\_6/ptodata/1/pna/US122\_COMB.seq:\*
- 43: /cgn2\_6/ptodata/1/pna/US123\_COMB.seq:\*

- 44: /cgn2\_6/ptodata/1/pna/US124\_COMB.seq:\*
- 45: /cgn2\_6/ptodata/1/pna/US125\_COMB.seq:\*
- 46: /cgn2\_6/ptodata/1/pna/US126\_COMB.seq:\*
- 47: /cgn2\_6/ptodata/1/pna/US127\_COMB.seq:\*
- 48: /cgn2\_6/ptodata/1/pna/US128\_COMB.seq:\*
- 49: /cgn2\_6/ptodata/1/pna/US129\_COMB.seq:\*
- 50: /cgn2\_6/ptodata/1/pna/US130\_COMB.seq:\*
- 51: /cgn2\_6/ptodata/1/pna/US131\_COMB.seq:\*
- 52: /cgn2\_6/ptodata/1/pna/US132\_COMB.seq:\*
- 53: /cgn2\_6/ptodata/1/pna/US133\_COMB.seq:\*
- 54: /cgn2\_6/ptodata/1/pna/US134\_COMB.seq:\*
- 55: /cgn2\_6/ptodata/1/pna/US135\_COMB.seq:\*
- 56: /cgn2\_6/ptodata/1/pna/US136\_COMB.seq:\*
- 57: /cgn2\_6/ptodata/1/pna/US137\_COMB.seq:\*
- 58: /cgn2\_6/ptodata/1/pna/US138\_COMB.seq:\*
- 59: /cgn2\_6/ptodata/1/pna/US139\_COMB.seq:\*
- 60: /cgn2\_6/ptodata/1/pna/US140\_COMB.seq:\*
- 61: /cgn2\_6/ptodata/1/pna/US141\_COMB.seq:\*
- 62: /cgn2\_6/ptodata/1/pna/US142\_COMB.seq:\*
- 63: /cgn2\_6/ptodata/1/pna/US143\_COMB.seq:\*
- 64: /cgn2\_6/ptodata/1/pna/US144\_COMB.seq:\*
- 65: /cgn2\_6/ptodata/1/pna/US145\_COMB.seq:\*
- 66: /cgn2\_6/ptodata/1/pna/US146\_COMB.seq:\*
- 67: /cgn2\_6/ptodata/1/pna/US147\_COMB.seq:\*
- 68: /cgn2\_6/ptodata/1/pna/US148\_COMB.seq:\*
- 69: /cgn2\_6/ptodata/1/pna/US149\_COMB.seq:\*
- 70: /cgn2\_6/ptodata/1/pna/US150\_COMB.seq:\*
- 71: /cgn2\_6/ptodata/1/pna/US151\_COMB.seq:\*
- 72: /cgn2\_6/ptodata/1/pna/US152\_COMB.seq:\*
- 73: /cgn2\_6/ptodata/1/pna/US153\_COMB.seq:\*
- 74: /cgn2\_6/ptodata/1/pna/US154\_COMB.seq:\*
- 75: /cgn2\_6/ptodata/1/pna/US155\_COMB.seq:\*
- 76: /cgn2\_6/ptodata/1/pna/US156\_COMB.seq:\*
- 77: /cgn2\_6/ptodata/1/pna/US157\_COMB.seq:\*
- 78: /cgn2\_6/ptodata/1/pna/US158\_COMB.seq:\*
- 79: /cgn2\_6/ptodata/1/pna/US159\_COMB.seq:\*
- 80: /cgn2\_6/ptodata/1/pna/US160\_COMB.seq:\*
- 81: /cgn2\_6/ptodata/1/pna/US161\_COMB.seq:\*
- 82: /cgn2\_6/ptodata/1/pna/US162\_COMB.seq:\*
- 83: /cgn2\_6/ptodata/1/pna/US163\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sun Apr 16 12:42:18 2006

us-09-9:

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 23:49:41 ; Search time 1329 Seconds  
(without alignments)  
9202.716 Million cell updates/sec

Title: US-09-991-518C-4  
Perfect score: 1479  
Sequence: 1 agagtttgatcctggctcag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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